

QY 223 ALASISSV 230
DB 98 ALASISSV 105

RESULT 5
MUTL_SALTI STANDARD; PRT; 618 AA.
AC Q82167;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA mismatch repair protein mutL.
GN MUTL OR STY4716 OR T4410.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=501;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Bauman D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Kirov S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Mcle S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.,
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. Jr., Mayhew G.F., Rose D.J.,
RA Burland V., Kocoyanni V., Schwarz D.C., Blattner F.R.,
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).

-1- FUNCTION: This protein is involved in the repair of mismatches in
DNA. It is required for dam-dependent methyl-directed DNA mismatch
repair. May act as a "molecular matchmaker", a protein that
promotes the formation of a stable complex between two or more
DNA-binding proteins in an ATP-dependent manner without itself
being part of a final effector complex. (By similarity).
-1- SIMILARITY: Belongs to the DNA mismatch repair mutL/hexB family.

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EMBL; AL627283; CAD06836.1; --
EMBL; AE016849; AAC71859.1; --
HAMAP; MF_00149; -- 1.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR002099; DNA_mis_repair.
Pfam; PF01119; DNA_mis_repair; 1.
Pfam; PF02518; HATPase_c; 1.
SMART; SM00387; HATPase_c; 1.
TIGRFAMs; TIGR00585; mutL; 1.
PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
DNA repair; Complete proteome.
SEQUENCE 618 AA; 67829 MW; 18DD90043D5180F4 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 223 ALASISSV 230
DB 98 ALASISSV 105

RESULT 6
MUTL_SALTY STANDARD; PRT; 618 AA.
AC P14161;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA mismatch repair protein mutL.
GN MUTL OR STM4359.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=9008766; PubMed=2676972;
RA Mankovich J.A., McIntyre C.A., Walker G.C.,
RT "Nucleotide sequence of the Salmonella typhimurium mutL gene required
for mismatch repair: homology of MutL to HexB of Streptococcus
pneumoniae and to PMS1 of the yeast Saccharomyces cerevisiae.";
RL J. Bacteriol. 171:5325-5331(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.,
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).

-1- FUNCTION: This protein is involved in the repair of mismatches in
DNA. It is required for dam-dependent methyl-directed DNA mismatch
repair. May act as a "molecular matchmaker", a protein that
promotes the formation of a stable complex between two or more
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-1- SIMILARITY: Belongs to the DNA mismatch repair mutL/hexB family.

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EMBL; M29687; AAA27166.1; --
EMBL; AE008904; AAL23179.1; --
PIR; A33588; A33588.
HSSP; P23367; 1B62.
StyGene; SG10236; mutL.
HAMAP; MF_00149; -- 1.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR002099; DNA_mis_repair.
Pfam; PF01119; DNA_mis_repair; 1.
Pfam; PF02518; HATPase_c; 1.
SMART; SM00387; HATPase_c; 1.
TIGRFAMs; TIGR00585; mutL; 1.
PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
DNA repair; Complete proteome.
SEQUENCE 618 AA; 67762 MW; 2896CA26AD358584 CRC64;

Exhibit A (page 2 of 2)

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Query Match 2.5%; Score 8; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY (320) 223 ALASISSV 230
DB (618) 98 ALASISSV 105

RESULT 7
MUTL CHLTE STANDARD; PRT; 624 AA.
AC Q8RA73 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA mismatch repair protein mutL
CN MUTL OR CT2028
OS Chlorobium tepidum.
OC Bacteria; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OC NCBI_TaxID=1097;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901;
RA Eison J.A., Nelson K.E., Paulsen I.T., Heidelberg J.P., Wu M.,
RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Kolonay J.L., Yang F.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RA "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium."
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
CC -!- FUNCTION: This protein is involved in the repair of mismatches in
CC DNA. It is required for dam-dependent methyl-directed DNA mismatch
CC repair. May act as a "molecular matchmaker", a protein that
CC promotes the formation of a stable complex between two or more
CC DNA-binding proteins in an ATP-dependent manner without itself
CC being part of a final effector complex (By similarity).
CC -!- SIMILARITY: Belongs to the DNA mismatch repair mutL/hexB family.
CC
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CC
CC EMBL; AE012953; AAY73245.1; -
CC TIGR; CT2028; -
CC HAMAP; MF_00149; -; 1.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR002099; DNA_mis_repair.
CC Pfam; PF01119; DNA_mis_repair; 1.
CC Pfam; PF02518; HATPase_c; 1.
CC TIGRFAMs; TIGR00585; mutL; 1.
CC PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
CC DNA repair; Complete proteome.
CC SEQUENCE 624 AA; 69836 MW; 43F3CE8214A42CFF CRC64;

Query Match 2.5%; Score 8; DB 1; Length 624;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 ALASISSV 230
DB 99 ALASISSV 106

RESULT 8
MUTL HASIN STANDARD; PRT; 629 AA.
AC P44494;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA mismatch repair protein mutL
CN MUTL OR H10067
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OC NCBI_TaxID=727;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT rd."
RL Science 269:496-512 (1995).
CC -!- FUNCTION: This protein is involved in the repair of mismatches in
CC DNA. It is required for dam-dependent methyl-directed DNA mismatch
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CC
CC EMBL; U32692; AAC21745.1; -
CC PIR; E64046; E64046.
CC HSSP; P23367; LBXN.
CC TIGR; H10067; -
CC HAMAP; MF_00149; -; 1.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR002099; DNA_mis_repair.
CC Pfam; PF01119; DNA_mis_repair; 1.
CC Pfam; PF02518; HATPase_c; 1.
CC SMART; SM00387; HATPase_c; 1.
CC TIGRFAMs; TIGR00585; mutL; 1.
CC PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
CC DNA repair; Complete proteome.
CC SEQUENCE 629 AA; 71622 MW; 0ADC240FD94D1556 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 629;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 ALASISSV 230
DB 98 ALASISSV 105

RESULT 9
MUTL PSEPK STANDARD; PRT; 632 AA.
AC Q88DD1;
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RESULT 8
MUTL HASIN STANDARD; PRT; 629 AA.
AC P44494;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA mismatch repair protein mutL
CN MUTL OR H10067
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OC NCBI_TaxID=727;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
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RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
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CC
CC EMBL; U32692; AAC21745.1; -
CC PIR; E64046; E64046.
CC HSSP; P23367; LBXN.
CC TIGR; H10067; -
CC HAMAP; MF_00149; -; 1.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR002099; DNA_mis_repair.
CC Pfam; PF01119; DNA_mis_repair; 1.
CC Pfam; PF02518; HATPase_c; 1.
CC SMART; SM00387; HATPase_c; 1.
CC TIGRFAMs; TIGR00585; mutL; 1.
CC PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
CC DNA repair; Complete proteome.
CC SEQUENCE 629 AA; 71622 MW; 0ADC240FD94D1556 CRC64;

Query Match 2.5%; Score 8; DB 1; Length 629;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 ALASISSV 230
DB 98 ALASISSV 105

RESULT 9
MUTL PSEPK STANDARD; PRT; 632 AA.
AC Q88DD1;
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